



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 06:46 pm GMT

PDB ID : 5J5O  
Title : Translation initiation factor 4E in complex with m7GppppG mRNA 5' cap analog  
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Deposited on : 2016-04-03  
Resolution : 1.87 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

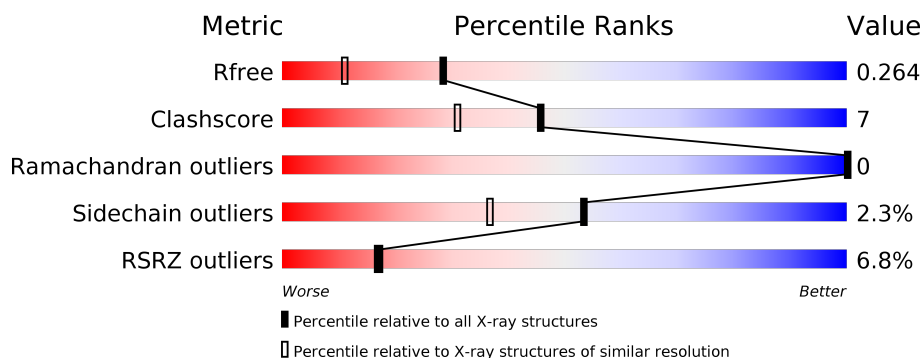
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.87 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	111664	2111 (1.86-1.86)
Clashscore	122126	2258 (1.86-1.86)
Ramachandran outliers	120053	2234 (1.86-1.86)
Sidechain outliers	120020	2234 (1.86-1.86)
RSRZ outliers	108989	2075 (1.86-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	190	<div> <div>81%</div> <div>14%</div> <div>5%</div> </div>
1	B	190	<div> <div>86%</div> <div>9%</div> <div>5%</div> </div>
1	C	190	<div> <div>12%</div> <div>75%</div> <div>18%</div> <div>6%</div> </div>
1	D	190	<div> <div>14%</div> <div>71%</div> <div>23%</div> <div>6%</div> </div>

2 Entry composition ⓘ

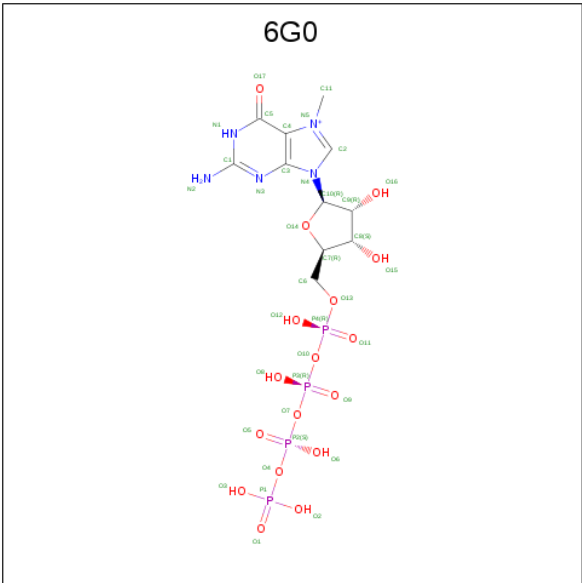
There are 4 unique types of molecules in this entry. The entry contains 6401 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Eukaryotic translation initiation factor 4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	0	6	0
			1514	971	260	277	6			
1	B	181	Total	C	N	O	S	0	5	0
			1496	963	253	274	6			
1	C	179	Total	C	N	O	S	0	4	0
			1461	937	245	273	6			
1	D	179	Total	C	N	O	S	0	5	0
			1409	894	244	265	6			

- Molecule 2 is 5'-O-[(R)-hydroxy{[(R)-hydroxy{[(S)-hydroxy(phosphonooxy)phosphoryl]oxy}phosphoryl]oxy}phosphoryl]-7-methylguanosine (three-letter code: 6G0) (formula: C<sub>11</sub>H<sub>20</sub>N<sub>5</sub>O<sub>17</sub>P<sub>4</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			37	11	5	17	4		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			37	11	5	17	4		
2	C	1	Total	C	N	O	P	0	0
			37	11	5	17	4		
2	D	1	Total	C	N	O	P	0	0
			37	11	5	17	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

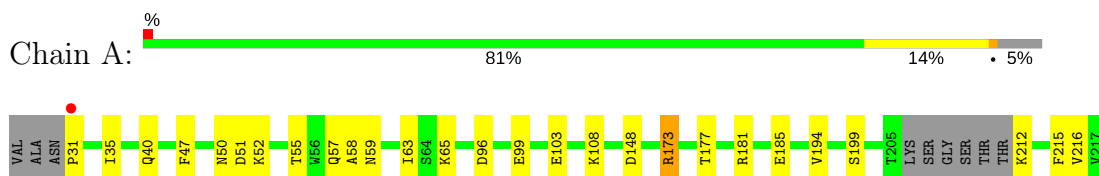
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	134	Total	O	0	2
			136	136		
4	B	126	Total	O	0	5
			131	131		
4	C	52	Total	O	0	1
			53	53		
4	D	41	Total	O	0	0
			41	41		

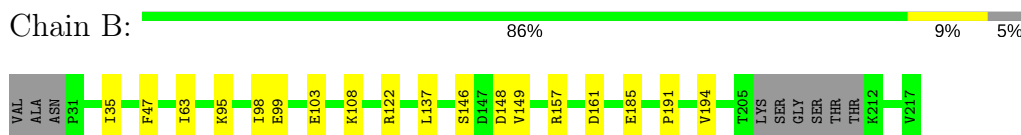
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

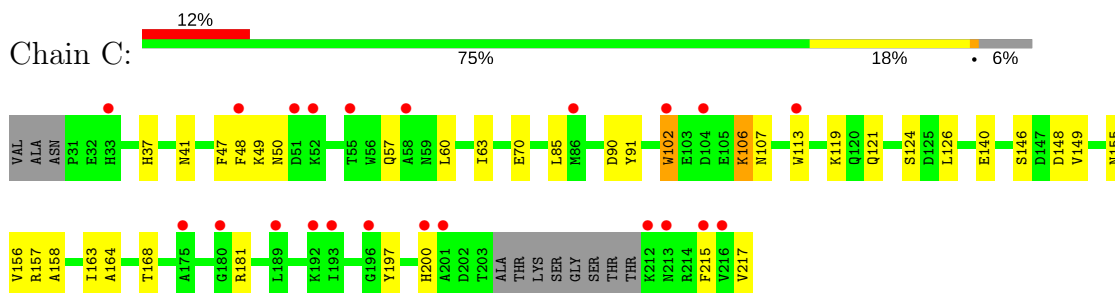
- Molecule 1: Eukaryotic translation initiation factor 4E



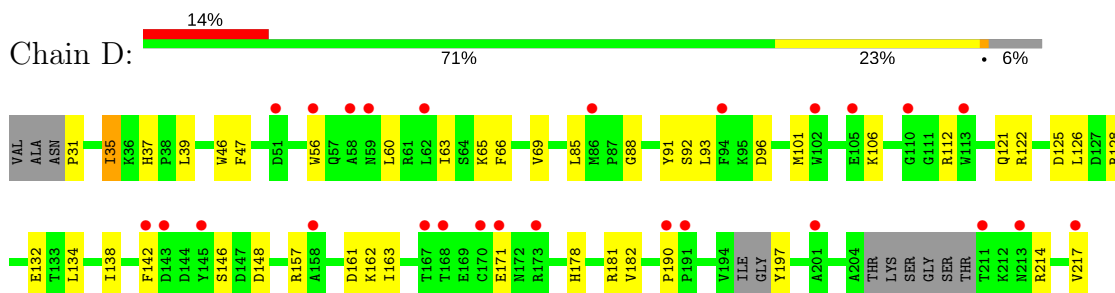
- Molecule 1: Eukaryotic translation initiation factor 4E



- Molecule 1: Eukaryotic translation initiation factor 4E



- Molecule 1: Eukaryotic translation initiation factor 4E



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	37.99Å 38.03Å 146.64Å 88.55° 84.70° 76.67°	Depositor
Resolution (Å)	36.82 – 1.87 36.82 – 1.87	Depositor EDS
% Data completeness (in resolution range)	91.2 (36.82-1.87) 81.8 (36.82-1.87)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.63 (at 1.87Å)	Xtriage
Refinement program	PHENIX (1.10_2152: ???)	Depositor
R, $R_{free}$	0.221 , 0.263 0.221 , 0.264	Depositor DCC
$R_{free}$ test set	2234 reflections (3.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.9	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.064 for -h,-k,-h+l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6401	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.24% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 6G0

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.47	1/1571 (0.1%)	0.65	0/2127
1	B	0.47	1/1546 (0.1%)	0.62	0/2094
1	C	0.33	0/1505	0.54	0/2045
1	D	0.34	0/1452	0.53	0/1973
All	All	0.41	2/6074 (0.0%)	0.59	0/8239

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	99	GLU	C-N	7.06	1.47	1.34
1	A	99	GLU	C-N	6.00	1.45	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1514	0	1475	19	0
1	B	1496	0	1442	13	0
1	C	1461	0	1364	21	0
1	D	1409	0	1298	29	0
2	A	37	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	37	0	0	0	0
2	C	37	0	0	0	0
2	D	37	0	0	0	0
3	A	6	0	8	0	0
3	B	6	0	8	2	0
4	A	136	0	0	5	0
4	B	131	0	0	2	0
4	C	53	0	0	3	1
4	D	41	0	0	2	0
All	All	6401	0	5595	80	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 80 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:LYS:NZ	4:A:401:HOH:O	2.16	0.78
1:D:65:LYS:NZ	1:D:96:ASP:OD2	2.20	0.73
1:D:132:GLU:OE1	4:D:401:HOH:O	2.14	0.65
1:D:181:ARG:HA	1:D:217:VAL:HG11	1.76	0.65
1:C:106:LYS:NZ	4:C:402:HOH:O	2.25	0.65

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:409:HOH:O	4:C:416:HOH:O[1_545]	2.09	0.11

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	183/190 (96%)	181 (99%)	2 (1%)	0	100	100
1	B	182/190 (96%)	176 (97%)	6 (3%)	0	100	100
1	C	179/190 (94%)	169 (94%)	10 (6%)	0	100	100
1	D	178/190 (94%)	169 (95%)	9 (5%)	0	100	100
All	All	722/760 (95%)	695 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	164/169 (97%)	160 (98%)	4 (2%)	52	35
1	B	158/169 (94%)	156 (99%)	2 (1%)	71	61
1	C	152/169 (90%)	148 (97%)	4 (3%)	49	32
1	D	142/169 (84%)	138 (97%)	4 (3%)	47	29
All	All	616/676 (91%)	602 (98%)	14 (2%)	53	37

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	60	LEU
1	C	102	TRP
1	D	146	SER
1	B	148	ASP
1	D	35	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	213	ASN
1	D	198	GLN
1	C	155	ASN

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Mol	Chain	Res	Type
1	B	155	ASN
1	C	80	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	6G0	A	301	-	29,39,39	1.26	2 (6%)	31,63,63	1.74	9 (29%)
3	GOL	A	302	-	5,5,5	0.40	0	5,5,5	0.36	0
2	6G0	B	301	-	29,39,39	1.24	3 (10%)	31,63,63	1.76	6 (19%)
3	GOL	B	302	-	5,5,5	0.30	0	5,5,5	0.25	0
2	6G0	C	300	-	29,39,39	1.19	2 (6%)	31,63,63	1.76	7 (22%)
2	6G0	D	300	-	29,39,39	1.20	2 (6%)	31,63,63	1.88	7 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	6G0	A	301	-	-	0/24/44/44	0/3/3/3
3	GOL	A	302	-	-	0/4/4/4	0/0/0/0
2	6G0	B	301	-	-	0/24/44/44	0/3/3/3
3	GOL	B	302	-	-	0/4/4/4	0/0/0/0
2	6G0	C	300	-	-	0/24/44/44	0/3/3/3
2	6G0	D	300	-	-	0/24/44/44	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	6G0	O14-C10	2.20	1.44	1.41
2	D	300	6G0	P1-O1	3.28	1.61	1.50
2	B	301	6G0	P1-O1	3.31	1.61	1.50
2	A	301	6G0	P1-O1	3.31	1.61	1.50
2	C	300	6G0	P1-O1	3.32	1.61	1.50

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	300	6G0	N3-C1-N1	-4.71	120.50	127.41
2	B	301	6G0	N3-C1-N1	-4.47	120.85	127.41
2	C	300	6G0	N3-C1-N1	-4.35	121.04	127.41
2	A	301	6G0	N3-C1-N1	-4.27	121.14	127.41
2	B	301	6G0	C4-C5-N1	-4.18	117.52	123.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	6G0	1	0
3	B	302	GOL	2	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	181/190 (95%)	-0.34	1 (0%) 89 90	12, 21, 38, 68	0
1	B	181/190 (95%)	-0.27	0 100 100	11, 21, 38, 66	0
1	C	179/190 (94%)	0.70	22 (12%) 4 4	22, 46, 88, 102	0
1	D	179/190 (94%)	0.80	26 (14%) 2 2	20, 48, 82, 101	0
All	All	720/760 (94%)	0.22	49 (6%) 17 17	11, 31, 77, 102	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	201	ALA	5.6
1	D	110	GLY	5.1
1	D	213	ASN	4.4
1	D	211	THR	4.4
1	C	189	LEU	4.3

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	6G0	D	300	37/37	0.76	0.21	47,75,89,93	0
2	6G0	C	300	37/37	0.88	0.17	28,61,80,83	0
3	GOL	B	302	6/6	0.94	0.09	25,33,35,42	0
3	GOL	A	302	6/6	0.96	0.08	27,31,32,33	0
2	6G0	A	301	37/37	0.97	0.07	14,21,52,60	0
2	6G0	B	301	37/37	0.97	0.08	8,19,51,61	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.